

OIPE

112

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/833,117

DATE: 05/02/2001

TIME: 12:21:03

Input Set : A:\PF543SL.txt

Output Set: N:\CRF3\05022001\I833117.raw

95

ENTERED

3 <110> APPLICANT: Rosen, Craig A.  
4 Sadeghi, Homa  
5 Prior, Christopher P.  
6 Turner, Andrew J.  
8 <120> TITLE OF INVENTION: Albumin Fusion Proteins  
10 <130> FILE REFERENCE: PF543  
C--> 12 <140> CURRENT APPLICATION NUMBER: US/09/833,117  
13 <141> CURRENT FILING DATE: 2001-04-12  
15 <150> PRIOR APPLICATION NUMBER: 60/229,358  
16 <151> PRIOR FILING DATE: 2000-04-12  
18 <150> PRIOR APPLICATION NUMBER: 60/256,931  
19 <151> PRIOR FILING DATE: 2000-12-21  
21 <150> PRIOR APPLICATION NUMBER: 60/199,384  
22 <151> PRIOR FILING DATE: 2000-04-25  
24 <160> NUMBER OF SEQ ID NOS: 36  
26 <170> SOFTWARE: PatentIn Ver. 2.1  
28 <210> SEQ ID NO: 1  
29 <211> LENGTH: 23  
30 <212> TYPE: DNA  
31 <213> ORGANISM: Artificial Sequence  
33 <220> FEATURE:  
34 <221> NAME/KEY: primer\_bind  
35 <223> OTHER INFORMATION: primer useful to clone human growth hormone cDNA  
37 <400> SEQUENCE: 1  
38 cccaagaatt cccttatcca ggc 23  
41 <210> SEQ ID NO: 2  
42 <211> LENGTH: 33  
43 <212> TYPE: DNA  
44 <213> ORGANISM: Artificial Sequence  
46 <220> FEATURE:  
47 <221> NAME/KEY: primer\_bind  
48 <223> OTHER INFORMATION: primer useful to clone human growth hormone cDNA  
50 <400> SEQUENCE: 2  
51 qqqaagctta qaagccacag gataccctcca cag 33  
54 <210> SEQ ID NO: 3  
55 <211> LENGTH: 16  
56 <212> TYPE: DNA  
57 <213> ORGANISM: Artificial Sequence  
59 <220> FEATURE:  
60 <221> NAME/KEY: misc\_structure  
61 <223> OTHER INFORMATION: synthetic oligonucleotide used to join DNA fragments  
62 with non-cohesive ends.  
64 <400> SEQUENCE: 3  
65 gataaagatt cccaac 16  
68 <210> SEQ ID NO: 4  
69 <211> LENGTH: 17  
70 <212> TYPE: DNA

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71 <213> ORGANISM: Artificial Sequence
73 <220> FEATURE:
74 <221> NAME/KEY: misc_structure
75 <223> OTHER INFORMATION: synthetic oligonucleotide used to join DNA fragments
76     with non-cohesive ends.
78 <400> SEQUENCE: 4
79 aatttgttggg aatcttt.                               17
82 <210> SEQ ID NO: 5
83 <211> LENGTH: 17
84 <212> TYPE: DNA
85 <213> ORGANISM: Artificial Sequence
87 <220> FEATURE:
88 <221> NAME/KEY: misc_structure
89 <223> OTHER INFORMATION: synthetic oligonucleotide used to join DNA fragments
90     with non-cohesive ends.
92 <400> SEQUENCE: 5
93 ttaggttat tcccaac                                   17
96 <210> SEQ ID NO: 6
97 <211> LENGTH: 18
98 <212> TYPE: DNA
99 <213> ORGANISM: Artificial Sequence
101 <220> FEATURE:
102 <221> NAME/KEY: misc_structure
103 <223> OTHER INFORMATION: synthetic oligonucleotide used to join DNA fragments
104     with non-cohesive ends.
106 <400> SEQUENCE: 6
107 aatttgttggg aataagcc                               18
110 <210> SEQ ID NO: 7
111 <211> LENGTH: 24
112 <212> TYPE: PRT
113 <213> ORGANISM: Artificial Sequence
115 <220> FEATURE:
116 <221> NAME/KEY: SITE
117 <222> LOCATION: 1)..(19)
118 <223> OTHER INFORMATION: invertase leader sequence
120 <220> FEATURE:
121 <221> NAME/KEY: SITE
122 <222> LOCATION: 20)..(24)
123 <223> OTHER INFORMATION: first 5 amino acids of mature human serum albumin
125 <400> SEQUENCE: 7
126 Met Leu Leu Gln Ala Phe Leu Phe Leu Leu Ala Gly Phe Ala Ala Lys
127   1           5           10           15
129 Ile Ser Ala Asp Ala His Lys Ser
130           20
133 <210> SEQ ID NO: 8
134 <211> LENGTH: 21
135 <212> TYPE: DNA
136 <213> ORGANISM: Artificial Sequence
138 <220> FEATURE:

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139 <221> NAME/KEY: misc structure
140 <223> OTHER INFORMATION: synthetic oligonucleotide used to join DNA
141     fragments with non-cohesive ends.
143 <400> SEQUENCE: 8
144 qagatgcaca cctqagtgag g                                21
147 <210> SEQ ID NO: 9
148 <211> LENGTH: 27
149 <212> TYPE: DNA
150 <213> ORGANISM: Artificial Sequence
152 <220> FEATURE:
153 <221> NAME/KEY: misc_structure
154 <223> OTHER INFORMATION: synthetic oligonucleotide used to join DNA
155     fragments with non-cohesive ends.
157 <400> SEQUENCE: 9
158 gatcctgttg cctcgatgca cacaaga                                27
161 <210> SEQ ID NO: 10
162 <211> LENGTH: 24
163 <212> TYPE: DNA
164 <213> ORGANISM: Artificial Sequence
166 <220> FEATURE:
167 <221> NAME/KEY: misc_structure
168 <223> OTHER INFORMATION: synthetic oligonucleotide used to join DNA
169     fragments with non-cohesive ends.
171 <400> SEQUENCE: 10
172 ctcttgtgtg catcgaaacc acag                                24
175 <210> SEQ ID NO: 11
176 <211> LENGTH: 30
177 <212> TYPE: DNA
178 <213> ORGANISM: Artificial Sequence
180 <220> FEATURE:
181 <221> NAME/KEY: misc_structure
182 <223> OTHER INFORMATION: synthetic oligonucleotide used to join DNA
183     fragments with non-cohesive ends.
185 <400> SEQUENCE: 11
186 tgttgaagag cctcagaatt tattcccaac                                30
189 <210> SEQ ID NO: 12
190 <211> LENGTH: 31
191 <212> TYPE: DNA
192 <213> ORGANISM: Artificial Sequence
194 <220> FEATURE:
195 <221> NAME/KEY: misc_structure
196 <223> OTHER INFORMATION: synthetic oligonucleotide used to join DNA
197     fragments with non-cohesive ends.
199 <400> SEQUENCE: 12
200 aatttgttgg aataaattct gagqctcttc c                                31
203 <210> SEQ ID NO: 13
204 <211> LENGTH: 47
205 <212> TYPE: DNA
206 <213> ORGANISM: Artificial Sequence

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208 <220> FEATURE:
209 <221> NAME/KEY: misc_structure
210 <223> OTHER INFORMATION: synthetic oligonucleotide used to join DNA
211     fragments with non-cohesive ends.
213 <400> SEQUENCE: 13
214 ttaaggettag gtggcgggtg atccggcgggt ggtggatctt tcccaac           47
217 <210> SEQ ID NO: 14
218 <211> LENGTH: 48
219 <212> TYPE: DNA
220 <213> ORGANISM: Artificial Sequence
222 <220> FEATURE:
223 <221> NAME/KEY: misc_structure
224 <223> OTHER INFORMATION: synthetic oligonucleotide used to join DNA
225     fragments with non-cohesive ends.
227 <400> SEQUENCE: 14
228 aattgttggg aaagatccac caccggcggg tccaccgcca cctaugcc           48
231 <210> SEQ ID NO: 15
232 <211> LENGTH: 62
233 <212> TYPE: DNA
234 <213> ORGANISM: Artificial Sequence
236 <220> FEATURE:
237 <221> NAME/KEY: misc_structure
238 <223> OTHER INFORMATION: synthetic oligonucleotide used to join DNA
239     fragments with non-cohesive ends.
241 <400> SEQUENCE: 15
242 ttaaggettag ggggtggtg atctggtagg ggcggatctg gtggcgggtg atccttccca 60
243 ac                                                                 62
246 <210> SEQ ID NO: 16
247 <211> LENGTH: 63
248 <212> TYPE: DNA
249 <213> ORGANISM: Artificial Sequence
251 <220> FEATURE:
252 <221> NAME/KEY: misc_structure
253 <223> OTHER INFORMATION: synthetic oligonucleotide used to join DNA
254     fragments with non-cohesive ends.
256 <400> SEQUENCE: 16
257 aattgttggg aaagatccac cccaccgga tccggcggc ccaagatccac caccgctaa 60
258 gcc                                                                 63
261 <210> SEQ ID NO: 17
262 <211> LENGTH: 1782
263 <212> TYPE: DNA
264 <213> ORGANISM: Homo sapiens
266 <220> FEATURE:
267 <221> NAME/KEY: CDS
268 <222> LOCATION: (1)..(1755)
271 <400> SEQUENCE: 17
272 gat gca cac aag aat gag gtt gct cat cgg ttt aaa gat ttg qga gaa   48
273 Asp Ala His Lys Ser Glu Val Ala His Arg Phe Lys Asp Leu Gly Glu
274 1          5          10          15

```

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```

276 gaa aat ttc aaa gcc ttg gtg ttg att gcc ttt gct cag tat ctt cag 96
277 Glu Asn Phe Lys Ala Leu Val Leu Ile Ala Phe Ala Gln Tyr Leu Gln
278          20          25          30
280 cag tgt cca ttt gaa gat cat gta aaa tta gtg aat gaa gta act gaa 144
281 Gln Cys Pro Phe Glu Asp His Val Lys Leu Val Asn Glu Val Thr Glu
282          35          40          45
284 ttt gca aaa aca tgt gtt gct gat gag tca gct gaa aat tgt gac aaa 192
285 Phe Ala Lys Thr Cys Val Ala Asp Glu Ser Ala Glu Asn Cys Asp Lys
286          50          55          60
288 tca ctt cat acc ctt ttt gga gac aaa tta tgc aca gtt gca act ctt 240
289 Ser Leu His Thr Leu Phe Gly Asp Lys Leu Cys Thr Val Ala Thr Leu
290 65          70          75          80
292 cgt gaa acc tat ggt gaa atg gct gac tgc tgt gca aaa caa gaa cct 288
293 Arg Glu Thr Tyr Gly Glu Met Ala Asp Cys Cys Ala Lys Gln Glu Pro
294          85          90          95
296 gag aqa aat gaa tgc ttc ttg caa cac aaa gat gac aac cca aac ctc 336
297 Glu Arg Asn Glu Cys Phe Leu Gln His Lys Asp Asp Asn Pro Asn Leu
298          100          105          110
300 ccc cga ttg gtg aga cca gag gtt gat gtg atg tgc act gct ttt cat 384
301 Pro Arg Leu Val Arg Pro Glu Val Asp Val Met Cys Thr Ala Phe His
302          115          120          125
304 gac aat gaa gag aca ttt ttg aaa aaa tac tta tat gaa att gcc aqa 432
305 Asp Asn Glu Glu Thr Phe Leu Lys Lys Tyr Leu Tyr Glu Ile Ala Arg
306          130          135          140
308 aqa cat cct tac ttt tat gcc ccg gaa ctc ctt ttc ttt gct aaa agg 480
309 Arg His Pro Tyr Phe Tyr Ala Pro Glu Leu Leu Phe Phe Ala Lys Arg
310 145          150          155          160
312 tat aaa gct gct ttt aca gaa tgt tgc caa gct gct gat aaa gct gcc 528
313 Tyr Lys Ala Ala Phe Thr Glu Cys Cys Gln Ala Ala Asp Lys Ala Ala
314          165          170          175
316 tgc ctg ttg cca aag ctc gat gaa ctt cgg gat gaa ggg aag gct tgg 576
317 Cys Leu Leu Pro Lys Leu Asp Glu Leu Arg Asp Glu Gly Lys Ala Ser
318          180          185          190
320 tct gcc aaa cag aqa ctc aaa tgt gcc aqt ctc caa aaa ttt gga gaa 624
321 Ser Ala Lys Gln Arg Leu Lys Cys Ala Ser Leu Gln Lys Phe Gly Glu
322          195          200          205
324 aqa gct ttc aaa gca tgg gca gtg gct cgc ctg agc cag aqa ttt ccc 672
325 Arg Ala Phe Lys Ala Trp Ala Val Ala Arg Leu Ser Gln Arg Phe Pro
326          210          215          220
328 aaa gct gag ttt gca gaa gtt tcc aag tta gtg aca gat ctt acc aaa 720
329 Lys Ala Glu Phe Ala Glu Val Ser Lys Leu Val Thr Asp Leu Thr Lys
330 225          230          235          240
332 gtc cac acg gaa tgc tgc cat gga gat ctg ctt gaa tgt gct gat gac 768
333 Val His Thr Glu Cys Cys His Gly Asp Leu Leu Glu Cys Ala Asp Asp
334          245          250          255
336 agg gcg gac ctt gcc aag tat atc tgt gaa aat cag gat tgg atc tcc 816
337 Arg Ala Asp Leu Ala Lys Tyr Ile Cys Glu Asn Gln Asp Ser Ile Ser
338          260          265          270
340 aqt aaa ctg aag gaa tgc tgt gaa aaa cct ctg ttg gaa aaa tcc cac 864

```

**Please Note:**

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

## VERIFICATION SUMMARY

PATENT APPLICATION: US/09/833,117

DATE: 05/02/2001

TIME: 12:21:04

Input Set : A:\PF543SL.txt

Output Set: N:\CRF3\05022001\I833117.raw

L:12 M:270 C: Current Application Number differs. Replaced Current Application Number  
L:710 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:25  
L:799 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:26  
L:888 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:27  
L:978 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:28  
L:1182 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:32  
L:1285 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:33